

<u>File Name</u>	<u>Date Created</u>	<u>Size (bytes).</u>
MakeHelp.bat	09/27/2000	1,594
newlibrarynamedlg.cpp	10/05/2000	1,926
newlibrarynamedlg.h	09/29/2000	883
resource.h	02/06/2001	8,530
resource.hm	02/06/2001	4,528
startdlg.cpp	10/23/2000	3,742
startdlg.h	10/23/2000	1,093
StdAfx.cpp	10/11/2000	221
StdAfx.h	10/03/2000	602
SubtractionLibraryUtility.cpp	10/11/2000	4,047
SubtractionLibraryUtility.h	02/06/2001	6,385
SubtractionLibraryUtility.hpj	02/06/2001	2,624
SubtractionLibraryUtility.rc	07/25/2001	28,316
SubtractionLibraryUtilityDlg.cpp	06/21/2001	209,771
SubtractionLibraryUtilityDlg.h	04/16/2001	6,943
SubtractionLibraryUtility.hm	08/09/2001	663
TimedMessage.cpp	10/27/2000	1,718
TimedMessage.h	10/27/2000	875
trimdialog.cpp	11/06/2000	119,594
trimdialog.h	11/06/2000	4,099
TUTORIAL PRIMERS.VEC	06/08/2001	2,039
TUTORIAL001.Seq	06/11/2001	640

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Replace the paragraph at page 8, line 3, with the following paragraph:

--BRIEF DESCRIPTION OF THE DRAWING

Fig. 1 shows a file directory structure for one embodiment of the invention.

Fig. 2 shows a Main User Interface computer display.

Fig. 3 (SEQ ID NOS 7, 9 and 12-16) shows a Trimming Interface computer display.--

Replace Table 2. beginning on page 18 with the following rewritten Table 2.

--Table 2.

Schlager's BLAST UTILITY, RESECO @1999
Results from file \\r5840\pub\MolTox\blast\TRIMMED\MB2D\M2r02_NV.SEQ
BLAST search done 4/5/2000

HTTP/1.0 200 OK MIME-Version: 1.0 Content-type: text/html

The query sequence for this search has been filtered. Filtering eliminates low complexity regions that commonly give spuriously high scores that reflect compositional bias rather than significant position-by-position alignment. Filtering can eliminate these potentially confounding matches (e.g., hits against proline-rich regions or poly-A tails) from the blast reports, leaving regions whose blast statistics reflect the specificity of their pairwise alignment.

BLASTN 2.0.11 [Jan-20-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= RESECO BLAST

UTILITY:\\r5840\pub\MolTox\blast\TRIMMED\MB2D\M2r02_NV.SEQ
(561 letters)

Database: nt

607,850 sequences; 1,816,255,750 total letters

	<u>Score</u>	<u>E</u>
Sequences producing significant alignments:		
gi 3228368 gb K02061.1 MUSRPL4A Mus musculus L32-4A pseudog...	565	e-159
gi 6981481 ref NM_013226.1 Rattus norvegicus ribosomal pr...	452	e-125

gi|3228368|gb|K02061.1|MUSRPL4A Mus musculus L32-4A pseudogene, complete seq
Length = 1516

Score = 565 bits (285), Expect = e-159

Identities = 360/384 (93%), Gaps = 5/384 (1%)

Strand = Plus / Minus

Query: SEQ ID NO: 1

38 gcagggttttgtgattttatttaaacataaaacatgcacacaagccatctactcattttct 97
|||||

Sbjct: SEQ ID NO: 2

1094 gcagggttttgtgattttatttaaacataaaacatgcacacaagccatctattcattttct 1035

Query: 98 tcgctgcgtancctggcggttgggattgggtgactctgatggccagctgtgctgctctttct 157
|||||

Sbjct: 1034 tcgctgcgtagcctggcggttgggattgggtgactctgatggccagctgtgctgctctttct 975

Query: 158 acaatggccttttcagttcttanaggacacattgtgagcaatctcagcacagtaagatttg 217
|||||

Sbjct: 974 acaatggccttttcggttcttagaggacacattgtgagcaatctcagcacagtaagatttg 915

Query: 218 ttgcacatcagcagcacctccagctccttgacattgtggaccannaacttgcggaanccg 277
|||||

Sbjct: 914 ttgcacatcagcagcacctccagctccttgacattgtggaccaggaacttgcggaanccg 855

Query: 278 ctgggcagcatgtgcttgggttttcttgttgcctccacaaccgaagtttnggcacangat 337
 |||||
 Sbjct: 854 ctgggcagcatgtgcttgggttttcttgttgcctccataaccgatg-ttgggcacaggat 796
 Query: 338 ntggcccttgaaccttctcc-cncctgttgcctatgcctctgggtttccnc--atttcn 394
 |||||
 Sbjct: 795 ctggcccttgaaccttctccgcacccctgttgcctatgcctctgggtttccgccagtttcg 736
 Query: 395 cttaa-tttcccatatcggtctga 417
 |||||
 Sbjct: 735 cttaattttcacatatcggtctga 712

gi|6981481|ref|NM_013226.1|| Rattus norvegicus ribsml protein L32(Rp132), mRNA

Length = 465

Score = 452 bits (228), Expect = e-125

Identities = 319/350 (91%), Gaps = 2/350 (0%)

Strand = Plus / Minus

Query: SEQ ID NO: 3

38 gcagggtttgtgattttatttaaacataaaacatgcacacaagccatctactcattttct 97
 |||||

Sbjct: SEQ ID NO: 4

461 gcagtttttgtggttttatttgaacacaaaacaggcacacaagccatctattcatttctct 402

Query: 98 tcgctgcgtancctggcggttgggattggtgactctgatggccagctgtgctgctctttct 157
 |||||

Sbjct: 401 tcgctgcgtagcctggcggttgggattggtgactctgatggccagctgtgctgctctttct 342

Query: 158 acaatggcttttcagttcttanaggacacattgtgagcaatctcagcacagtaagatttg 217
 |||||

Sbjct: 341 acgatggcttttcggttcttagaggacacattgtgagcaatctcagcacagtaagatttg 282

Query: 218 ttgcacatcagcagcacctccagctccttgacattgtggaccannaacttgcggaanccg 277
 |||||

Sbjct: 281 ttgcacatcagcagcacttccagctccttgacattgtggaccagaaacttccggaagccg 222

Query: 278 ctgggcagcatgtgcttgggttttcttgttgcctccacaaccgaagtttnggcacangat 337
 |||||

Sbjct: 221 ctaggcagcatgtgcttgggttttcttgttactcccgtacc-aatgttgggcacaggat 163

Query: 338 ntggcccttgaaccttctcc-cncctgttgcctatgcctctgggtttcc 386
 |||||

Sbjct: 162 ctggcccttgaatcttctccgcacccctgttgcctatgcctctgggtttcc 113

Database: nt

Posted date: Mar 30, 2000 10:02 PM

Number of letters in database: 1,816,255,750

Number of sequences in database: 607,850

Lambda K H
 1.37 0.711 0.00

Gapped

Lambda K H
 1.37 0.711 4.94e-324

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 420761

Number of Sequences: 607850

Number of extensions: 420761

Number of successful extensions: 34073

Number of sequences better than 10.0: 52

length of query: 561

length of database: 1,816,255,750

effective HSP length: 20
 effective length of query: 541
 effective length of database: 1,804,098,750
 effective search space: 976017423750
 effective search space used: 976017423750

T: 0

A: 0

X1: 6 (11.9 bits)

X2: 10 (19.8 bits)

S1: 12 (24.3 bits)

S2: 19 (38.2 bits)

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Replace the label for Table 3. at page 20, line 8, with the following label:

N.G. 7--Table 3. (SEQ ID NO: 5)--
 Where.

Replace the paragraph at page 24, line 7 with the following paragraph:

-- A vector file must be customized for a particular laboratory and selected prior to the trimming step. The vectors files are formatted using a six line, ASCII text format. Only the first contiguous string of letters on each line is read, so the remainder of each line can be used for annotations. Each line starts with a nucleotide sequence. An example vector file is presented below (SEQ ID NOS 6-11, respectively in order of appearance):

AGCGGCCGCCCCGGGCAGGTC // positive insertion orientation 5' adapter sequence

ACCTCGGCCGCGACCAAGCT // positive insertion orientation 3' adapter sequence

TTACTAGTGGATCCGAGCTCGGTACCAAGCTTC // forward direction confirm
 fragment 25 bases after 3' adapter

AGCGTGGTCGCGGCCGAGGT // negative insertion orientation 5' adapter sequence

ACCTGCCCCGGGCGGCCGCTC // negative insertion orientation 3' adapter sequence

CACACTGGCGGCCGCTCGAGCATGCATCTAGAG // reverse direction confirm fragment
 25 bases after 3' adapter. --